



SEQUENCE LISTING

<110> LALANNE, JEAN L
ROCHER, CORINNE

<120> Novel genes of Candida albicans and the proteins coded
by these genes

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<140> 09/980,054

<141> 2001-11-28

<150> FR 9907250

<151> 1999-06-09

<150> PCT/FR00/01567

<151> 2000-06-08

<160> 32

<170> PatentIn Ver. 2.1

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tcc aaa ggc att caa gat tta gaa aat cgt tta aac gga tta ggt tat	336
Ser Lys Gly Ile Gln Asp Leu Glu Asn Arg Leu Asn Gly Leu Gly Tyr	
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Glu Lys Ser Gln Asp Leu Pro Asn Glu Tyr Met Ile Val Glu Asn Val	
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Pro Leu Leu Asn Arg Phe Ile Ser Ile Pro Lys Glu Tyr Gly Asp Leu	
180 185 190	
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Asn Cys Ser Ala Phe Val Ala Gly Ile Ile Glu Gly Ala Leu Asp Asn	
195 200 205	
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Ser Gly Phe Asn Ala Asp Val Thr Ala His Thr Val Ala Thr Asp Ala	
210 215 220	
aat cca tta aga aca gta ttt ttg atc aag ttt gac gat tct gtt tta	720
Asn Pro Leu Arg Thr Val Phe Leu Ile Lys Phe Asp Asp Ser Val Leu	
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 Tyr Asp Arg Asn Ile Ile Thr Lys Lys Pro His Glu Ile Asn Leu Ser
 65 70 75 80
 Ser Leu Ser Phe Leu Phe Cys Glu Ile Ile Ser Trp Ala His Ser Asn
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 Ser Lys Gly Ile Gln Asp Leu Glu Asn Arg Leu Asn Gly Leu Gly Tyr
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 Glu Lys Ser Gln Asp Leu Pro Asn Glu Tyr Met Ile Val Glu Asn Val
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 Lys Gln Asp Leu Met Ser Thr Val Leu Thr Met Met Ser Asn Gln Gln
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 Gly Val Leu Ser Gly Asp Phe Lys Leu Gln Leu Met Ile Ile Glu Thr
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 Asp Leu Glu Arg Leu Asn Tyr Ile Val Arg Leu Tyr Ile Arg Thr Arg
 100 105 110
 ttg agt aag ttg aat aaa ttt act att ttt tac atc aat gaa agc agt 384
 Leu Ser Lys Leu Asn Lys Phe Thr Ile Phe Tyr Ile Asn Glu Ser Ser
 115 120 125
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 130 135 140

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Tyr Phe Gln Ile Leu Thr Gln Leu Tyr Asn Asn Cys Phe Leu Lys Lys
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180 185 190

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Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp	
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Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu	
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Leu	Lys	Glu	Lys	Lys	Val	Ser	Arg	Trp	Arg	Gln	Lys	Gln	Gln	Gln	Glu	
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Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp	
100 105 110	
cat gaa cac aat gga cat gct cat gaa cat gca gag gga tac cat gga	384
His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly	
115 120 125	
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Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln	
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Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val	
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Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp	
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340 345 350	
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Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His	
355 360 365	
aaa tac agt ata cta cca aaa aca gac tca gat gat cag agt ttt aca	1152
Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr	
370 375 380	
gat gaa atc aaa caa cta tca ctt gac ttt gaa gat atg atg tgg gac	1200
Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp	
385 390 395 400	
ttg ata gac caa tta cga atc att gaa aca ata aca gag gca gct gat	1248
Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp	
405 410 415	
gaa aaa aag acc aga aac tta tct gtc aga aat tat gca ata gag gca	1296
Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala	
420 425 430	
ttg tgg tta tat aga act gga ggt gga aga cca gag ata act aaa caa	1344
Leu Trp Leu Tyr Arg Thr Gly Gly Gly Arg Pro Glu Ile Thr Lys Gln	
435 440 445	
acc gaa gag gat ttg ata gca caa gca gtt cag aaa taa	1383
Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys	
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<213> Candida albicans

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20 25 30

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35 40 45

Gln Ser Thr Thr Ser Pro Lys Thr Thr Glu Ile Arg Ser Glu Ala Ser
50 55 60

Lys Ile His Gln Glu Asn Ile Glu Lys Met Ala Gln Met Ser Glu Glu
65 70 75 80

Glu Ile Leu Gln Glu Arg Glu Glu Leu Leu Lys Gly Leu Asp Pro Lys
85 90 95

Leu Ile Glu Ser Leu Ile Gly Arg Ser Lys Lys Arg Glu Ala Thr Asp
100 105 110

His Glu His Asn Gly His Ala His Glu His Ala Glu Gly Tyr His Gly
115 120 125

Trp Ile Gly Ser Met Lys Thr Ser Glu Gly Leu Thr Asp Leu Ser Gln
130 135 140

Leu Asp Lys Glu Asp Val Asp Arg Ala Leu Gly Ile Ser Ser Leu Ser
145 150 155 160

Leu Ser Glu Pro Glu Gly Gly Ser Asn Thr Lys Lys Val Ala Phe Asp
165 170 175

Asp Asn Ile Lys Thr Val Lys Phe Glu Ala Leu Asp Asp Glu Ile Glu
180 185 190

Leu Asp Pro Asn Gly Trp Glu Asp Val Thr Asp Val Asn Glu Leu Val
195 200 205

Pro Asn Asn Asp His Ile Ala Pro Asp Asp Tyr Gln Ile Asn Pro Asp

210	215	220
Ser Asp Glu Glu Gly Leu Asn Asn Thr Val His Phe Thr Lys Pro Lys		
225	230	235 240
Gln Pro Asp Leu Asp Ile Asn Asp Pro Asp Phe Phe Asp Lys Leu His		
	245	250 255
Glu Lys Tyr Tyr Pro Asp Leu Pro Lys Glu Thr Glu Lys Leu Ser Trp		
	260	265 270
Met Thr Gln Pro Met Pro Lys Gln Leu Ser Thr Val Tyr Glu Ser Ile		
	275	280 285
Ser Asp Met Arg Phe Asp Phe Lys Gly Asp Leu Ile Glu Leu Ser Ala		
	290	295 300
Glu Gly Glu Glu Pro Lys Asp Ser Ser Phe Glu Ile Pro Thr Tyr Met		
	305	310 315 320
Gly Leu His His His Ser Glu Asn Pro His Met Ala Gly Tyr Thr Leu		
	325	330 335
Gly Glu Leu Ala His Leu Ala Arg Ser Thr Leu Ala Gly Gln Arg Cys		
	340	345 350
Leu Ser Ile Gln Thr Leu Gly Arg Ile Leu His Lys Leu Gly Leu His		
	355	360 365
Lys Tyr Ser Ile Leu Pro Lys Thr Asp Ser Asp Asp Gln Ser Phe Thr		
	370	375 380
Asp Glu Ile Lys Gln Leu Ser Leu Asp Phe Glu Asp Met Met Trp Asp		
	385	390 395 400
Leu Ile Asp Gln Leu Arg Ile Ile Glu Thr Ile Thr Glu Ala Ala Asp		
	405	410 415
Glu Lys Lys Thr Arg Asn Leu Ser Val Arg Asn Tyr Ala Ile Glu Ala		
	420	425 430
Leu Trp Leu Tyr Arg Thr Gly Gly Gly Arg Pro Glu Ile Thr Lys Gln		
	435	440 445
Thr Glu Glu Asp Leu Ile Ala Gln Ala Val Gln Lys		
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 cag cat gtt aca ggt gcc agg ttc cgt cag cga aaa atc tcg gta aag 96
 Gln His Val Thr Gly Ala Arg Phe Arg Gln Arg Lys Ile Ser Val Lys
 20 25 30
 cag ccc ttg act att tat aaa cag aga gac cta cct act cta gat agc 144
 Gln Pro Leu Thr Ile Tyr Lys Gln Arg Asp Leu Pro Thr Leu Asp Ser
 35 40 45
 aat gag tta gag cct agt caa gtc cat cat tta aat tct aat gcg tca 192
 Asn Glu Leu Glu Pro Ser Gln Val His His Leu Asn Ser Asn Ala Ser
 50 55 60
 tca tca tca aca caa caa ccc aga gac ctt cat gca gtt gaa act ggg 240
 Ser Ser Ser Thr Gln Gln Pro Arg Asp Leu His Ala Val Glu Thr Gly
 65 70 75 80
 gtt gac aag aat gag gaa gag gaa gtg cat ctt cag caa gtt atc aat 288
 Val Asp Lys Asn Glu Glu Glu Glu Val His Leu Gln Gln Val Ile Asn
 85 90 95
 gct gca caa aaa gca ctt ttg ggt tgg aaa aaa gaa gaa aaa agc agt 336
 Ala Ala Gln Lys Ala Leu Leu Gly Ser Lys Lys Glu Glu Lys Ser Ser
 100 105 110
 gat atg tat att ccc aca ccc gac gct tgg agg ata tgg ccc gag gca 384

Asp Met Tyr Ile Pro Thr Pro Asp Ala Ser Arg Ile Trp Pro Glu Ala	
115 120 125	
cac aag tat tac aag gat caa aag ttc aag cag cca gag aca tat atc	432
His Lys Tyr Tyr Lys Asp Gln Lys Phe Lys Gln Pro Glu Thr Tyr Ile	
130 135 140	
aag ttt agt gcg aca gta gag gac aca gtg ggt gtg gag tac aat atg	480
Lys Phe Ser Ala Thr Val Glu Asp Thr Val Gly Val Glu Tyr Asn Met	
145 150 155 160	
gac gag gta gat gaa aag ttt tat aga gag aca cta tgc aag tac tat	528
Asp Glu Val Asp Glu Lys Phe Tyr Arg Glu Thr Leu Cys Lys Tyr Tyr	
165 170 175	
ccc aaa aag aaa aac aag tca gat gag aac aat cga aag tgt act gaa	576
Pro Lys Lys Lys Asn Lys Ser Asp Glu Asn Asn Arg Lys Cys Thr Glu	
180 185 190	
ttg gag ttt gaa aca atc tgt gac aag ttg gaa aag acc att gaa gca	624
Leu Glu Phe Glu Thr Ile Cys Asp Lys Leu Glu Lys Thr Ile Glu Ala	
195 200 205	
cga caa ccg ttt ttg tct atg gac ccc agc aac att cta tgc tac gag	672
Arg Gln Pro Phe Leu Ser Met Asp Pro Ser Asn Ile Leu Ser Tyr Glu	
210 215 220	
gag ttg tgg tgg tac att gtg gat cag ttc aaa agt gca gtg aaa aca	720
Glu Leu Ser Ser Tyr Ile Val Asp Gln Phe Lys Ser Ala Val Lys Thr	
225 230 235 240	
agc aac ccg tat att gtt acc aat ggt ggg aat cta gag tat ata tgg	768
Ser Asn Pro Tyr Ile Val Thr Asn Gly Gly Asn Leu Glu Tyr Ile Ser	
245 250 255	
acg aca gct tta aaa gag aga ttg tgg aag gaa ata aag tat gaa ccg	816
Thr Thr Ala Leu Lys Glu Arg Leu Ser Lys Glu Ile Lys Tyr Glu Pro	
260 265 270	
ttt gtt act att ttt gat aag aac caa atg tcc aca agt gcg gtg aga	864
Phe Val Thr Ile Phe Asp Lys Asn Gln Met Ser Thr Ser Ala Val Arg	
275 280 285	
ccc att ccc aaa ttg ttt gag ttg ttc ggc aga cct gtt tat gat cat	912
Pro Ile Pro Lys Leu Phe Glu Leu Phe Gly Arg Pro Val Tyr Asp His	
290 295 300	
ttg aag gag aga aaa ata gaa aga aag ggc aaa acc atc cag ccc aca	960

Trp Lys Glu Arg Lys Ile Glu Arg Lys Gly Lys Thr Ile Gln Pro Thr	
305 310 315 320	
ctc aaa ttt gag gat cct aac tgg aac gaa aag gaa aac gac aat gac	1008
Leu Lys Phe Glu Asp Pro Asn Ser Asn Glu Lys Glu Asn Asp Asn Asp	
325 330 335	
cca tat ata tgt ttc aga cga cgt gag ttt agg caa gca aga aag acg	1056
Pro Tyr Ile Cys Phe Arg Arg Arg Glu Phe Arg Gln Ala Arg Lys Thr	
340 345 350	
aga aga gcc gat aca att ggt gca gag aga ata aga ctg atg caa aag	1104
Arg Arg Ala Asp Thr Ile Gly Ala Glu Arg Ile Arg Leu Met Gln Lys	
355 360 365	
tgg ttg cac cgc gca cgt gat ttg ata atg agt gtt agt gaa aga gag	1152
Ser Leu His Arg Ala Arg Asp Leu Ile Met Ser Val Ser Glu Arg Glu	
370 375 380	
atc ctc aaa ctc gac aat ttt caa gca gag cat gaa ttg ttt aaa gcc	1200
Ile Leu Lys Leu Asp Asn Phe Gln Ala Glu His Glu Leu Phe Lys Ala	
385 390 395 400	
agg tgc gct acc aag gct tgt aag agg gag ctc aat atc aag ggt gac	1248
Arg Cys Ala Thr Lys Ala Cys Lys Arg Glu Leu Asn Ile Lys Gly Asp	
405 410 415	
gaa tac ttg ttc ttt cgg cat aaa aag aag aaa att gtt cgt act gaa	1296
Glu Tyr Leu Phe Phe Pro His Lys Lys Lys Lys Ile Val Arg Thr Glu	
420 425 430	
gat gaa gaa agg gag aag aag aga gaa aag aag aag caa gac caa gaa	1344
Asp Glu Glu Arg Glu Lys Lys Arg Glu Lys Lys Lys Gln Asp Gln Glu	
435 440 445	
ctt gca ctc aag caa caa caa gca cta cag caa cag cag caa caa cca	1392
Leu Ala Leu Lys Gln Gln Gln Ala Leu Gln Gln Gln Gln Gln Gln Pro	
450 455 460	
cca caa cca cca caa caa gca cca tca aaa caa gat ggt aca tca acg	1440
Pro Gln Pro Pro Gln Gln Ala Pro Ser Lys Gln Asp Gly Thr Ser Thr	
465 470 475 480	
agc cag cct tat gtc aaa ctc cca ccc gra aaa gtt cca gat atg gat	1488
Ser Gln Pro Tyr Val Lys Leu Pro Pro Ala Lys Val Pro Asp Met Asp	
485 490 495	
ctt gtt aca gtt tgg ttg gta tta aag gaa aag aac gaa acc atc aaa	1536

Leu Val Thr Val Ser Leu Val Leu Lys Glu Lys Asn Glu Thr Ile Lys	
500	505 510
cgt gct gtg ttg gag aaa ttg cgc aag aga aag gaa cac gar aag gga	1584
Arg Ala Val Leu Glu Lys Leu Arg Lys Arg Lys Glu His Asp Lys Gly	
515	520 525
ttt atc aat ttg aca gat gat cgc tat cag cca ttt ttc gat att tca	1632
Phe Ile Asn Leu Thr Asp Asp Pro Tyr Gln Pro Phe Phe Asp Ile Ser	
530	535 540
acc aat agg gcc gaa gag ttg agc cat att cgc tat tgc tgc att gcc	1680
Thr Asn Arg Ala Glu Glu Leu Ser His Ile Pro Tyr Ser Ser Ile Ala	
545	550 555 560
gcc aca cac tat cac caa ttc aac aca tgc aac tac atg aac gac caa	1728
Ala Thr His Tyr His Gln Phe Asn Thr Ser Asn Tyr Met Asn Asp Gln	
565	570 575
ctt aaa aag cta ctt gaa gag aaa aaa cct tta cct ggt gta aaa acg	1776
Leu Lys Lys Leu Leu Glu Glu Lys Lys Pro Leu Pro Gly Val Lys Thr	
580	585 590
ttt ttg ggt tct aac ggg gag ttg gta cca tgc aag gca ttt cca cat	1824
Phe Leu Gly Ser Asn Gly Glu Leu Val Pro Ser Lys Ala Phe Pro His	
595	600 605
ttg ctg tgc ttg ctt gag gaa aag tat aag gcc aca agt ggg tat att	1872
Leu Leu Ser Leu Leu Glu Glu Lys Tyr Lys Ala Thr Ser Gly Tyr Ile	
610	615 620
gaa cga tta ttg caa agc gtg gag acg caa gat ttt agt tca tac acc	1920
Glu Arg Leu Leu Gln Ser Val Glu Thr Gln Asp Phe Ser Ser Tyr Thr	
625	630 635 640
aat gcc ttt aaa gat gtt gag cca aaa gaa aca aat gaa cct gtt atg	1968
Asn Gly Phe Lys Asp Val Glu Pro Lys Glu Thr Asn Glu Pro Val Met	
645	650 655
ggc ttt ccc cag aga ata cgt cga aga gtg ggc agg gct ggc agg gtt	2016
Ala Phe Pro Gln Arg Ile Arg Arg Arg Val Gly Arg Ala Gly Arg Val	
660	665 670
ttt ttg gac cac cag caa gag tac cgc caa cgc aat ttt cag caa gac	2064
Phe Leu Asp His Gln Gln Glu Tyr Pro Gln Pro Asn Phe Gln Gln Asp	
675	680 685
aca gat cgt gtg gga ggt atc cca gat gtg tat tgt aaa gag gat gcc	2112

Thr Asp Arg Val Gly Gly Ile Pro Asp Val Tyr Cys Lys Glu Asp Ala
 690 695 700

att aaa cga tta cag tca aag tgg aag ttc gat aca gaa tat aaa aca 2160
 Ile Lys Arg Leu Gln Ser Lys Trp Lys Phe Asp Thr Glu Tyr Lys Thr
 705 710 715 720

att gaa cca ttt agt ttg gat cct tca aag ttg aat ggt att agt cca 2208
 Thr Glu Pro Phe Ser Leu Asp Pro Ser Lys Leu Asn Gly Ile Ser Pro
 725 730 735

ttt aag caa tgg att aga ttt ggg tct atg ttg ttg aat aga aca cct 2256
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 740 745 750

aaa tag 2262
 Lys

<210> 10
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 <213> Candida albicans

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 20 25 30
 Gln Pro Leu Thr Ile Tyr Lys Gln Arg Asp Leu Pro Thr Leu Asp Ser
 35 40 45
 Asn Glu Leu Glu Pro Ser Gln Val His His Leu Asn Ser Asn Ala Ser
 50 55 60
 Ser Ser Ser Thr Gln Gln Pro Arg Asp Leu His Ala Val Glu Thr Gly
 65 70 75 80
 Val Asp Lys Asn Glu Glu Glu Val His Leu Gln Gln Val Ile Asn
 85 90 95
 Ala Ala Gln Lys Ala Leu Leu Gly Ser Lys Lys Glu Glu Lys Ser Ser
 100 105 110
 Asp Met Tyr Ile Pro Thr Pro Asp Ala Ser Arg Ile Trp Pro Glu Ala
 115 120 125
 His Lys Tyr Tyr Lys Asp Gln Lys Phe Lys Gln Pro Glu Thr Tyr Ile
 130 135 140
 Lys Phe Ser Ala Thr Val Glu Asp Thr Val Gly Val Glu Tyr Asn Met
 145 150 155 160
 Asp Glu Val Asp Glu Lys Phe Tyr Arg Glu Thr Leu Cys Lys Tyr Tyr
 165 170 175
 Pro Lys Lys Lys Asn Lys Ser Asp Glu Asn Asn Arg Lys Cys Thr Glu

	180		185		190
Leu Glu Phe Glu Thr Ile Cys Asp Lys	Leu Glu Lys Thr Ile Glu Ala				
195	200	205			
Arg Gln Pro Phe Leu Ser Met Asp Pro Ser Asn Ile Leu Ser Tyr Glu					
210	215	220			
Glu Leu Ser Ser Tyr Ile Val Asp Gln Phe Lys Ser Ala Val Lys Thr					
225	230	235			240
Ser Asn Pro Tyr Ile Val Thr Asn Gly Gly Asn Leu Glu Tyr Ile Ser					
245	250	255			
Thr Thr Ala Leu Lys Glu Arg Leu Ser Lys Glu Ile Lys Tyr Glu Pro					
260	265	270			
Phe Val Thr Ile Phe Asp Lys Asn Gln Met Ser Thr Ser Ala Val Arg					
275	280	285			
Pro Ile Pro Lys Leu Phe Glu Leu Phe Gly Arg Pro Val Tyr Asp His					
290	295	300			
Trp Lys Glu Arg Lys Ile Glu Arg Lys Gly Lys Thr Ile Gln Pro Thr					
305	310	315			320
Leu Lys Phe Glu Asp Pro Asn Ser Asn Glu Lys Glu Asn Asp Asn Asp					
325	330	335			
Pro Tyr Ile Cys Phe Arg Arg Arg Glu Phe Arg Gln Ala Arg Lys Thr					
340	345	350			
Arg Arg Ala Asp Thr Ile Gly Ala Glu Arg Ile Arg Leu Met Gln Lys					
355	360	365			
Ser Leu His Arg Ala Arg Asp Leu Ile Met Ser Val Ser Glu Arg Glu					
370	375	380			
Ile Leu Lys Leu Asp Asn Phe Gln Ala Glu His Glu Leu Phe Lys Ala					
385	390	395			400
Arg Cys Ala Thr Lys Ala Cys Lys Arg Glu Leu Asn Ile Lys Gly Asp					
405	410	415			
Glu Tyr Leu Phe Phe Pro His Lys Lys Lys Lys Ile Val Arg Thr Glu					
420	425	430			
Asp Glu Glu Arg Glu Lys Lys Arg Glu Lys Lys Lys Gln Asp Gln Glu					
435	440	445			
Leu Ala Leu Lys Gln Gln Gln Ala Leu Gln Gln Gln Gln Gln Pro					
450	455	460			
Pro Gln Pro Pro Gln Gln Ala Pro Ser Lys Gln Asp Gly Thr Ser Thr					
465	470	475			480
Ser Gln Pro Tyr Val Lys Leu Pro Pro Ala Lys Val Pro Asp Met Asp					
485	490	495			
Leu Val Thr Val Ser Leu Val Leu Lys Glu Lys Asn Glu Thr Ile Lys					
500	505	510			
Arg Ala Val Leu Glu Lys Leu Arg Lys Arg Lys Glu His Asp Lys Gly					
515	520	525			
Phe Ile Asn Leu Thr Asp Asp Pro Tyr Gln Pro Phe Phe Asp Ile Ser					
530	535	540			
Thr Asn Arg Ala Glu Glu Leu Ser His Ile Pro Tyr Ser Ser Ile Ala					
545	550	555			560
Ala Thr His Tyr His Gln Phe Asn Thr Ser Asn Tyr Met Asn Asp Gln					

	565		570		575
Leu Lys Lys	Leu Leu Glu Glu Lys Lys	Pro Leu Pro Gly Val Lys Thr			
	580	585	590		
Phe Leu Gly Ser Asn Gly Glu Leu Val	Pro Ser Lys Ala Phe Pro His				
	595	600	605		
Leu Leu Ser Leu Leu Glu Glu Lys Tyr Lys Ala Thr Ser Gly Tyr Ile					
	610	615	620		
Glu Arg Leu Leu Gln Ser Val Glu Thr Gln Asp Phe Ser Ser Tyr Thr					
625	630	635	640		
Asn Gly Phe Lys Asp Val Glu Pro Lys Glu Thr Asn Glu Pro Val Met					
	645	650	655		
Ala Phe Pro Gln Arg Ile Arg Arg Arg Val Gly Arg Ala Gly Arg Val					
	660	665	670		
Phe Leu Asp His Gln Gln Glu Tyr Pro Gln Pro Asn Phe Gln Gln Asp					
	675	680	685		
Thr Asp Arg Val Gly Gly Ile Pro Asp Val Tyr Cys Lys Glu Asp Ala					
	690	695	700		
Ile Lys Arg Leu Gln Ser Lys Trp Lys Phe Asp Thr Glu Tyr Lys Thr					
705	710	715	720		
Thr Glu Pro Phe Ser Leu Asp Pro Ser Lys Leu Asn Gly Ile Ser Pro					
	725	730	735		
Ser Thr Gln Ser Ile Arg Phe Gly Ser Met Leu Leu Asn Arg Thr Arg					
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Lys

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 <112> DNA
 <113> Candida albicans

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1 5 10 15														
tat gaa tta gga ttt aaa gaa ggt caa ata caa gga aca aaa gat caa	96													
Tyr Glu Leu Gly Phe Lys Glu Gly Gln Ile Gln Gly Thr Lys Asp Gln														
20 25 30														
tat tta gaa gga aaa gaa tat ggt tat caa act gga ttt caa cga ttt	144													
Tyr Leu Glu Gly Lys Glu Tyr Gly Tyr Gln Thr Gly Phe Gln Arg Phe														
35 40 45														

ttt atc att ggt tat att caa gaa tta atg aaa ttt tgg tta tcc cat	192
Leu Ile Ile Gly Tyr Ile Gln Glu Leu Met Lys Phe Trp Leu Ser His	
50 55 60	
ata gat caa tat aat aac tct tct tca cct cgg aat cat ttg aat aat	240
Ile Asp Gln Tyr Asn Asn Ser Ser Ser Leu Arg Asn His Leu Asn Asn	
65 70 75 80	
ttg gaa gat att atg gca caa att tct ata acg aat gga gat aaa gaa	288
Leu Glu Asp Ile Met Ala Gln Ile Ser Ile Thr Asn Gly Asp Lys Glu	
85 90 95	
gtt gaa gat tat gaa aaa aat att aaa aag gca aga aat aaa tta aga	336
Val Glu Asp Tyr Glu Lys Asn Ile Lys Lys Ala Arg Asn Lys Leu Arg	
100 105 110	
gtg ata gct agt ata act aaa gaa act tgg aaa att gat tca ttg gat	384
Val Ile Ala Ser Ile Thr Lys Glu Thr Trp Lys Ile Asp Ser Leu Asp	
115 120 125	
aat ttg gtg aaa gaa gta ggt gga act tta caa gtt agt gaa aac ccc	432
Asn Leu Val Lys Glu Val Gly Gly Thr Leu Gln Val Ser Glu Asn Pro	
130 135 140	
gat gat atg tgg tga	447
Asp Asp Met Trp	
145	

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 <112> PRT
 <113> Candida albicans

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Tyr Leu Glu Gly Lys Glu Tyr Gly Tyr Gln Thr Gly Phe Gln Arg Phe
35 40 45
Leu Ile Ile Gly Tyr Ile Gln Glu Leu Met Lys Phe Trp Leu Ser His
50 55 60
Ile Asp Gln Tyr Asn Asn Ser Ser Ser Leu Arg Asn His Leu Asn Asn
65 70 75 80
Leu Glu Asp Ile Met Ala Gln Ile Ser Ile Thr Asn Gly Asp Lys Glu
85 90 95

Val Glu Asp Tyr Glu Lys Asn Ile Lys Lys Ala Arg Asn Lys Leu Arg
 100 105 110
 Val Ile Ala Ser Ile Thr Lys Glu Thr Trp Lys Ile Asp Ser Leu Asp
 115 120 125
 Asn Leu Val Lys Glu Val Gly Gly Thr Leu Gln Val Ser Glu Asn Pro
 130 135 140
 Asp Asp Met Trp
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 1 5 10 15

 agt tca acc gat tca gaa act gaa tta gaa agc aca caa caa caa caa 96
 Ser Ser Thr Asp Ser Glu Thr Glu Leu Glu Ser Thr Gln Gln Gln Gln
 20 25 30

 caa caa caa gaa ggt gct act aca att caa gaa act gtt gat gtt gat 144
 Gln Gln Gln Glu Gly Ala Thr Thr Ile Gln Glu Thr Val Asp Val Asp
 35 40 45

 ttt gat ttt ttt gat tta aat cct caa att gat ttc cat gct act aag 192
 Phe Asp Phe Phe Asp Leu Asn Pro Gln Ile Asp Phe His Ala Thr Lys
 50 55 60

 aat ttt tta aga caa tta ttt ggt gat gat aat gga gaa ttt aat tta 240
 Asn Phe Leu Arg Gln Leu Phe Gly Asp Asp Asn Gly Glu Phe Asn Leu
 55 70 75 80

 agt gaa ata gcc gat tta att tta tga gaa aat tcc gtg ggg aca tca 288
 Ser Glu Ile Ala Asp Leu Ile Leu Arg Glu Asn Ser Val Gly Thr Ser
 85 90 95

 att aaa act gaa gga atg gaa agt gat tca ttt gca att tta agt gta 336
 Ile Lys Thr Glu Gly Met Glu Ser Asp Pro Phe Ala Ile Leu Ser Val
 100 105 110

att aat tta act aat aat tta aat gtg gcc gtg att aaa caa ttg att	384
Ile Asn Leu Thr Asn Asn Leu Asn Val Ala Val Ile Lys Gln Leu Ile	
115 120 135	
gaa tat att tca aat aaa acc aaa tct aaa act gaa ttc aat att att	432
Glu Tyr Ile Ser Asn Lys Thr Lys Ser Lys Thr Glu Phe Asn Ile Ile	
130 135 140	
ttg aaa aaa ttg tta acc aat cag aac gat act act aga gat agg aaa	480
Leu Lys Lys Leu Leu Thr Asn Gln Asn Asp Thr Thr Arg Asp Arg Lys	
145 150 155 160	
ttt aaa act gga tta ata att agt gaa aga ttt ata aat atg cca gtt	528
Phe Lys Thr Gly Leu Ile Ile Ser Glu Arg Phe Ile Asn Met Pro Val	
165 170 175	
gaa gtg att cca cca atg tat aaa atg ctt tta caa gaa atg gaa aaa	576
Glu Val Ile Pro Pro Met Tyr Lys Met Leu Leu Gln Glu Met Glu Lys	
180 185 190	
gct gaa gat gct cat gaa aat tat gaa ttt gat tat ttt tta att ata	624
Ala Glu Asp Ala His Glu Asn Tyr Glu Phe Asp Tyr Phe Leu Ile Ile	
195 200 205	
tca aga gtt tat caa tta gtt gat cca gtg gaa aga gaa gat gaa gat	672
Ser Arg Val Tyr Gln Leu Val Asp Pro Val Glu Arg Glu Asp Glu Asp	
210 215 220	
cac gaa aaa gaa tcc aat cgt aaa aag aag aac aag aat aag aag aag	720
His Glu Lys Glu Ser Asn Arg Lys Lys Lys Asn Lys Asn Lys Lys Lys	
225 230 235 240	
aaa ttg gct aat aat gaa cca aaa cca ata gaa atg gat tat ttc cat	768
Lys Leu Ala Asn Asn Glu Pro Lys Pro Ile Glu Met Asp Tyr Phe His	
245 250 255	
ctt gaa gat caa att ttg gaa tca aat act caa ttt aaa gga ata ttt	816
Leu Glu Asp Gln Ile Leu Glu Ser Asn Thr Gln Phe Lys Gly Ile Phe	
260 265 270	
gaa tat aat aat gaa aat aaa caa gaa aca gat tca aga aga gta ttt	864
Glu Tyr Asn Asn Glu Asn Lys Gln Glu Thr Asp Ser Arg Arg Val Phe	
275 280 285	
act gaa tat ggt att gat cct aaa tta agt tta atc tta att gat aaa	912
Thr Glu Tyr Gly Ile Asp Pro Lys Leu Ser Leu Ile Leu Ile Asp Lys	
290 295 300	

gat aat tta gct aaa tca gtc att gaa atg gaa caa caa ttc cca cct 960
 Asp Asn Leu Ala Lys Ser Val Ile Glu Met Glu Gln Gln Phe Pro Pro
 305 310 315 320

cca taa 966
 Pro

<210> 14
 <211> 321
 <212> PRT
 <213> Candida albicans

<400> 14
 Met Gly Lys Arg Arg Val Asp Glu Glu Ser Asp Ser Asp Ile Asp Val
 1 5 10 15
 Ser Ser Thr Asp Ser Glu Thr Glu Leu Glu Ser Thr Gln Gln Gln Gln
 20 25 30
 Gln Gln Gln Glu Gly Ala Thr Thr Ile Gln Glu Thr Val Asp Val Asp
 35 40 45
 Phe Asp Phe Phe Asp Leu Asn Pro Gln Ile Asp Phe His Ala Thr Lys
 50 55 60
 Asn Phe Leu Arg Gln Leu Phe Gly Asp Asp Asn Gly Glu Phe Asn Leu
 65 70 75 80
 Ser Glu Ile Ala Asp Leu Ile Leu Arg Glu Asn Ser Val Gly Thr Ser
 85 90 95
 Ile Lys Thr Glu Gly Met Glu Ser Asp Pro Phe Ala Ile Leu Ser Val
 100 105 110
 Ile Asn Leu Thr Asn Asn Leu Asn Val Ala Val Ile Lys Gln Leu Ile
 115 120 125
 Glu Tyr Ile Ser Asn Lys Thr Lys Ser Lys Thr Glu Phe Asn Ile Ile
 130 135 140
 Leu Lys Lys Leu Leu Thr Asn Gln Asn Asp Thr Thr Arg Asp Arg Lys
 145 150 155 160
 Phe Lys Thr Gly Leu Ile Ile Ser Glu Arg Phe Ile Asn Met Pro Val
 165 170 175
 Glu Val Ile Pro Pro Met Tyr Lys Met Leu Leu Gln Glu Met Glu Lys
 180 185 190
 Ala Glu Asp Ala His Glu Asn Tyr Glu Phe Asp Tyr Phe Leu Ile Ile
 195 200 205
 Ser Arg Val Tyr Gln Leu Val Asp Pro Val Glu Arg Glu Asp Glu Asp
 210 215 220
 His Glu Lys Glu Ser Asn Arg Lys Lys Lys Asn Lys Asn Lys Lys Lys
 225 230 235 240
 Lys Leu Ala Asn Asn Glu Pro Lys Pro Ile Glu Met Asp Tyr Phe His
 245 250 255
 Leu Glu Asp Gln Ile Leu Glu Ser Asn Thr Gln Phe Lys Gly Ile Phe

260	265	270
Glu Tyr Asn Asn Glu Asn Lys Gln Glu Thr Asp Ser Arg Arg Val Phe		
275	280	285
Thr Glu Tyr Gly Ile Asp Pro Lys Leu Ser Leu Ile Leu Ile Asp Lys		
290	295	300
Asp Asn Leu Ala Lys Ser Val Ile Glu Met Glu Gln Gln Phe Pro Pro		
305	310	315
Pro		320

<210> 15
 <211> 300
 <212> DNA
 <213> Candida albicans

<400> 15
 caatttatto atgggtcgggt ctggaaattg atttttggta aaactgctaa tgaattagaa 60
 aaatcgcaag atttgcctaa tgaatatatg attgtggaga atgtgccatt attaaataga 120
 tttattagta tacctaagga gtatggcgac ttaaattggt cagcatttgt tgcgggtata 180
 attgagggag cacttgataa tagtggatte aatgccgatg ttacagcaca caggttcgct 240
 acagatgcaa atccattaag aacagtatct ttgatcaagt ttgacgatcc tgttttaatt 300
 agagagagtt cgagatttgg 320

<210> 16
 <211> 295
 <212> DNA
 <213> Candida albicans

<400> 16
 gttcatggtt ggtgactcag agcgtctcaa ctatattggt cgattatata tacgaactcg 60
 attgagtaag ttgaataaat ttactatttt ttacatcaat gaaagcagtc aaaatgataa 120
 tttattgtcc aaagaggaaa gagattatat acacaaatat ttccagattt tgactcaatt 180
 atataacaa acgtttctca aaaaactaac acaaatgttg acctatttgg atgacaccag 240
 tgggtggaaa caaatgatcg ttgagccaga tttagaccag cctgtgttta tcaaa 295

<210> 17
 <211> 392
 <212> DNA
 <213> Candida albicans

<400> 17
 atctctgata tgagatttgg ctttaaaggg gatttaattg aattgggtcc agtgggagat 60
 gcaaccaag atagttcacc cgacatacgt actcatatgg gactccatca tcattcggag 120
 aacccacata tggcaggtta tacattgggt gagttggccc atttagccag atcgacttta 180
 gctggacaaa gatgcttagg cattcaaaaa ttaggggagaa tcttcacataa attgggatta 240

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cataaataca gtataatacc aaaccagctc aatgatcaga gttttacaga tgaatcaaaa 300
ctatacaattg accttgaaga tagatgtggg atttgataga ccaattaaga atcattgaaa 360
caataacaga ggcagctgat ggaaaaaaga cc 392

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<210> 18
 <211> 335
 <212> DNA
 <213> Candida albicans

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<400> 18
attccacac cggacgcttc gaggatatgg ccgagggcac acaagtatta caaggatcaa 60
aagttcaagc agccagagac atatatcaag tttagtggga cagtagagga cacagtgggt 120
gtggagtaca atatggagca ggtagatgaa aagttttata gagagacact atgcaagtac 180
tattccaaaa agaaaaacaa gtcagatgag aacaatcgaa agtgtactga attggagttt 240
gaaacaactc gtgacaagtt ggaaaagacc attgaagcac gacaaccgtt tttgtctatg 300
gacccacgca acattctatc gtaagaggag ttgtc 335

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<210> 19
 <211> 336
 <212> DNA
 <213> Candida albicans

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<400> 19
agatatagat aatgtattaa atttagaaga agatcaatat gaattaggat ttaaagaagg 60
tcaaatacaa ggaacaaaaag atcaatatat agaaggaaaa gaatatggtt atcaaatctg 120
attcaacga tttttaatac ttggttatat tcaagaatta atgaaatttt ggttatccca 180
tatagatcaa tataataact cttcttcaat tcggaatcat ttgaataatt tgggaagatat 240
tatggcagaa atttctataa cgaatggaga taaagaagtt gaagattatg aaaaaaatat 300
taaaaggcca agaaataaat taagag 336

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<210> 20
 <211> 374
 <212> DNA
 <213> Candida albicans

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<400> 20
ctttaaattg atttccatgc tactaagaat ttttaagaca ttatttggtg atgataatgg 60
agaatttaat ttaagtgaag tagccgattt aattttacga gaaaattccg tggggacatc 120
aattaaaaat gaaggaaatgg aaagtgatec atttgcaatt ttaagtgtaa ttaatttaac 180
taataattta aatgtggcgc tgattaaaca attgattgaa tatattttta ataaaaccaa 240
atctaaaaat gaattcaata ttattttgaa aaaattgtta accaatcaga acgatactac 300
tagagatagg aaatttaaaa ctggattaat aattagtgtg agattttata atatgccagt 360
tgaagtgatt ccac 374

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<210> 31
<211> 35
<212> DNA
<213> Candida albicans

<210>
<211> modified_base
<212> (18)
<213> a-a or g or c or t

<400> 31
aaattatc argttcgnat ctggaaattg atttt 25

<210> 32
<211> 29
<212> DNA
<213> Candida albicans

<400> 32
ccaaatcica aactctctct aattaaaac 29

<210> 23
<211> 38
<212> DNA
<213> Candida albicans

<400> 23
gttcattgtt ggtgaactcag agcgtctcaa ctatattg 38

<210> 24
<211> 33
<212> DNA
<213> Candida albicans

<400> 24
tttgataaac acagggttgg cttaaactcgg etc 33

<210> 25
<211> 32
<212> DNA
<213> Candida albicans

<400> 25
atctttgata tgagatttgg ctttaaaggg ga 32

<210> 35
<211> 31
<212> DNA
<213> Candida albicans

<400> 16
gggttttttt ccattcagctg cctctgttat tg

32

<210> 17
<211> 30
<212> DNA
<213> Candida albicans

<400> 17
attccacacac cggacgcttc

20

<210> 38
<211> 30
<212> DNA
<213> Candida albicans

<400> 28
gacaactcct cgtacgatag

20

<210> 29
<211> 30
<212> DNA
<213> Candida albicans

<400> 29
agataatgta ttaaatttag

20

<210> 30
<211> 30
<212> DNA
<213> Candida albicans

<400> 30
gcttaatttt atttcttggc

20

<210> 31

<211> 20
<212> DNA
<213> Candida albicans

<400> 31
cctcgaattg atttccatgc 20

<210> 32
<211> 20
<212> DNA
<213> Candida albicans

<400> 32
gtggaatcac ttcaactggc 20